

# SEQUENCE LISTING

<110> Hayward, Nicholas K.  
Weber, Gunther  
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Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
SAME

<130> DAVIES

<140> 08/765,588

<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 649

<212> DNA

<213> Nucleotide Sequence of VEGF165

<220>

<221> CDS

<222> (17)..(589)

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gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala	Leu	Leu	Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro
	15						20					25			

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met	Ala	Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met
	30					35				40					

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp
45					50					55				60	

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser
			65					70						75	

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg	292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg	340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag	388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa	436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa	484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln	
145 150 155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc	532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys	
160 165 170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag	580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys	
175 180 185	
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg	629
Pro Arg Arg	
190	
gaaccagatc tctcaccagg	649

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 <212> PRT  
 <213> Nucleotide Sequence of VEGF165

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 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
                   35                                  40                                  45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
           50                                  55                                  60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
   65                                  70                                  75                                  80  
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
                                   85                                  90                                  95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
                   100                                  105                                  110  
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
                   115                                  120                                  125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
   130                                  135                                  140  
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
 145                                  150                                  155                                  160  
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
                   165                                  170                                  175  
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg  
                   180                                  185                                  190

<210> 3  
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 <213> Nucleotide Sequence of SOM175

<220>  
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 <222> (3)..(623)

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       1                  5                  10                  15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                   20                  25                  30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
           35                  40                  45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
50 55 60  
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
65 70 75  
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
80 85 90 95  
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
100 105 110  
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
115 120 125  
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431  
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His  
130 135 140  
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479  
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala  
145 150 155  
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527  
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser  
160 165 170 175  
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575  
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala  
180 185 190  
gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623  
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
195 200 205  
tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683  
agactcagca ggggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803  
 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863  
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923  
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattcttaca actggctctt 983  
 cctccccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043  
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4  
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 <213> Nucleotide Sequence of SOM175

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 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
 130 135 140  
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 145 150 155 160  
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

	165		170		175										
His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Ala
			180					185					190		
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		195					200					205			

<210> 5  
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 <212> DNA  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>  
 <221> CDS  
 <222> (3)..(566)

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 1 5 10 15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
 20 25 30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
 35 40 45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
 50 55 60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
 65 70 75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
 80 85 90 95  
 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
 100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
 115 120 125  
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431  
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro  
 130 135 140  
 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479  
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys  
 145 150 155  
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527  
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu  
 160 165 170 175  
 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576  
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
 180 185  
 cttttcagac tcagcagggt gacttgccctc agaggctata tcccagtggg ggaacaaagg 636  
 ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696  
 gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tcctgagggc catcatcaaa 756  
 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816  
 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876  
 gctcttcttc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936  
 acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6  
 <211> 188  
 <212> PRT  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6  
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 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
                     35                    40                    45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
                     50                    55                    60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
                     65                    70                    75                    80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
                     85                    90                    95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
                     100                    105                    110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
                     115                    120                    125  
 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg  
                     130                    135                    140  
 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
                     145                    150                    155                    160  
 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu  
                     165                    170                    175  
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
                     180                    185

<210> 7  
 <211> 858  
 <212> DNA  
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>  
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 <222> (3)..(431)

<400> 7  
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     Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
       1                    5                    10                    15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30



cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
35 40 45  
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
50 55 60  
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
65 70 75  
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
80 85 90 95  
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
100 105 110  
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
115 120 125  
aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg 431  
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
130 135 140  
tgacacatgg cttttcagac tcagcaggggt gacttgcttc agaggctata tcccagtgagg 491  
ggaacaaagg ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa 551  
gctgctctag gacctgggcc tctcagaggg ctcttctgcc atcccttgctc tcctgagggc 611  
catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671  
ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat 731  
cttacaactg gctcttcttc ccctcactaa gaagacccaa acctctgcat aatgggattt 791  
gggctttggt acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa 851

aaaaaaa

858

<210> 8  
 <211> 143  
 <212> PRT  
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8  
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 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
                     20                    25                    30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
                     35                    40                    45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
                     50                    55                    60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
     65                    70                    75                    80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
                     85                    90                    95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
                     100                    105                    110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
                     115                    120                    125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
     130                    135                    140

<210> 9  
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 <212> DNA  
 <213> Nuc. Seq. of SOM175 Absent Exon 4

<220>  
 <221> CDS  
 <222> (3)..(305)

<400> 9  
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       1                    5                    10                    15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                             20                            25                            30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
                             35                            40                            45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
                             50                            55                            60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
                             65                            70                            75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
                             80                            85                            90                            95  
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgtg tgaagccaga 335  
 Gln Val Arg Met Gln Thr  
                             100  
 cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395  
 ccccgagca cctccccag ctgacatcac ccatccact ccagccccag gccctctgc 455  
 ccacgtgca ccagcacca ccagcgcct gacccccga cctgccgtg ccgctgccga 515  
 cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575  
 tgccggaagc tgcaaggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635  
 aggtatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695  
 cctcagcca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755  
 ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815  
 gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct ctcc

910

<210> 10  
<211> 101  
<212> PRT  
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10  
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
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20 25 30  
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45  
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60  
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80  
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95  
Val Arg Met Gln Thr  
100

<210> 11  
<211> 42  
<212> DNA  
<213> Oligonucleotide

<400> 11  
accaccacct ccctgggctg gcatgtggca cgtgcataaa cg

42

<210> 12  
<211> 42  
<212> DNA  
<213> Oligonucleotide

<400> 12  
agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13  
<211> 38  
<212> DNA

<213> Oligonucleotide

<400> 13

gacacctgggg ctggagtggg atggatgatg tcagctgg

38

<210> 14

<211> 40

<212> DNA

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<400> 14

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<211> 236

<212> DNA

<213> Human SOM175

<400> 15

atgagggggcc aggtacgtga ggtctccac agggccctgg aaagaatact tacatctgct 60

cccatggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctctccgta ggctgcctcc agccccaggc 180

ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

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<221> CDS

<222> (166)..(789)

<400> 16

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gggggcccgc gaggagccgc cccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcgggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177

Met Ser Pro Leu

1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu	Ala	Arg	Thr	Gln	
5					10					15					20	
gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40					45					50			
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
		55					60					65				
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggc	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
	70					75					80					
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
85					90					95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
				105					110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120					125					130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
		135					140					145				
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
	150					155					160					
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
165					170					175					180	
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

185                      190                      195  
 gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc 799  
 Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala  
                     200                      205  
 agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859  
 ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919  
 cagtctggga ggtcactgcc ccaggacctg gaccttttag agagctctct cgccatcttt 979  
 tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctgagggggc 1039  
 aggggtactct ctcaactaac caccctgggc aagtgagcat cttctggctg gctgtctccc 1099  
 ctcaactatga aaaccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact 1159  
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 aaaaaaaaaa aaaaaaaaaa aaa 1242

<210> 17  
 <211> 207  
 <212> PRT  
 <213> mVRF

<400> 17  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu  
   1                    5                    10                    15  
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln  
                     20                    25                    30  
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln  
                     35                    40                    45  
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val  
                     50                    55                    60  
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
                     65                    70                    75                    80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
                     85                    90                    95  
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly  
                     100                    105                    110  
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
                     115                    120                    125  
 Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg  
                     130                    135                    140

Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro
145					150					155					160
Ser	Pro	Ala	Asp	Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala
				165					170					175	
Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val
			180					185					190		
Ala	Ala	Val	Asp	Ala	Ala	Ala	Ser	Ile	Ala	Lys	Gly	Gly	Ala		
		195					200				205				

<210> 18  
 <211> 188  
 <212> PRT  
 <213> mVRF167

<400> 18															
Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu
1				5					10					15	
Ala	Arg	Thr	Gln	Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln
			20					25					30		
Lys	Lys	Val	Val	Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln
		35					40					45			
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val
		50				55					60				
Val	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
	65				70					75					80
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
				85					90					95	
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
			100					105					110		
Glu	Met	Ser	Leu	Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
		115					120					125			
Lys	Glu	Ser	Ala	Val	Arg	Pro	Asp	Ser	Pro	Arg	Ile	Leu	Cys	Pro	Pro
	130					135					140				
Cys	Thr	Gln	Arg	Arg	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg
145					150					155					160
Cys	Arg	Arg	Arg	Arg	Phe	Leu	His	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu
				165					170					175	
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Pro	Arg	Lys				
			180					185							

<210> 19  
 <211> 188



<212> PRT  
<213> hVRF167

<400> 19

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	Leu		
1				5					10					15			
Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln		
			20					25					30				
Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln		
		35					40					45					
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val		
	50					55					60						
Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly		
65					70					75					80		
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln		
				85					90					95			
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly		
			100					105					110				
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys		
		115					120					125					
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	Arg		
	130					135					140						
Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg		
145					150				155						160		
Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu		
				165					170					175			
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg						
			180					185									

<210> 20  
<211> 71  
<212> PRT  
<213> mVRF186

<400> 20

Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly		
1				5					10					15			
Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	Ile	Ile	His	Pro		
			20					25					30				
Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn		
		35					40					45					

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser  
50 55 60

Ser Ile Ala Lys Gly Gly Ala  
65 70

<210> 21  
<211> 71  
<212> PRT  
<213> hVRF186

<400> 21  
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly  
1 5 10 15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro  
20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser  
35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser  
50 55 60

Ser Val Ala Lys Gly Gly Ala  
65 70

<210> 22  
<211> 214  
<212> PRT  
<213> mVEGF188

<400> 22  
Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly  
20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg  
35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr  
50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met  
65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr  
85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln  
100 105 110

Ser	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Ser	Arg	Cys	Glu
		115					120					125			
Cys	Arg	Pro	Lys	Lys	Asp	Arg	Thr	Lys	Pro	Glu	Lys	Lys	Ser	Val	Arg
	130					135					140				
Gly	Lys	Gly	Lys	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Lys	Ser	Arg	Phe	Lys
145					150					155					160
Ser	Trp	Ser	Val	His	Cys	Glu	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu
				165					170					175	
Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp
			180					185					190		
Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg
		195					200					205			
Cys	Asp	Lys	Pro	Arg	Arg										
	210														